CLAIMS:

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- 1. An isolated or recombinant immunogenic polypeptide which comprises, mimics or cross-reacts with a B-cell or T-cell epitope of a *Lawsonia spp.* polypeptide selected from the group consisting of flhB, fliR, ntrC, glnH, motA, motB, tlyC, ytfM, and ytfN polypeptides.
- 2. The isolated or recombinant immunogenic polypeptide of claim 1 capable of eliciting the production of antibodies against *Lawsonia spp.* when administered to an avian or porcine animal.
- 3. The isolated or recombinant immunogenic polypeptide of claim 1 capable of conferring a protective immune response against *Lawsonia spp.* when administered to an avian or porcine animal.
- 15 4. The isolated or recombinant immunogenic polypeptide of claim 2 wherein the *Lawsonia spp.* is *L. intracellularis*.
 - 5. The isolated or recombinant immunogenic polypeptide of claim 3 wherein the *Lawsonia spp.* is *L. intracellularis*.
 - 6. An isolated or recombinant polypeptide selected from the group consisting of:
 - (i) a polypeptide of *Lawsonia spp.* which comprises an amino acid sequence which has at least about 60% sequence identity overall to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12,
- 25 14, 16, and 18;
 - (ii) a polypeptide of *Lawsonia spp*. which comprises an amino acid sequence which has at least about 60% sequence identity overall to an amino acid sequence encoded by *Lawsonia intracellularis* DNA contained within a plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480

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(plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN);

- (iii) a polypeptide which comprises at least about 5 contiguous amino acids of an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, and 18;
- (iv) a polypeptide which comprises at least about 5 contiguous amino acids of an amino acid sequence encoded by *Lawsonia intracellularis* DNA contained within a plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN); and
- (v) a polypeptide which comprises an amino acid sequence encoded by a nucleotide sequence of *Lawsonia spp.* having at least about 60% sequence identity overall to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, and 17;
- (vi) a polypeptide which comprises an amino acid sequence encoded by a nucleotide sequence of *Lawsonia spp.* having at least about 60% sequence identity overall to the nucleotide sequence of *Lawsonia intracellularis* DNA contained within a plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN);
- (vii) a polypeptide encoded by at least about 15 contiguous nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, and 17;
- (viii) a polypeptide encoded by at least about 15 contiguous nucleotides of a nucleotide sequence of *Lawsonia intracellularis* DNA contained within a plasmid

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selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN); and (ix) a homologue, analogue or derivative of any one of (i) to (vii) which mimics a B-cell or T-cell epitope of *Lawsonia spp*.

- 7. The isolated or recombinant polypeptide of claim 6 capable of eliciting the production of antibodies against *Lawsonia spp.* in a porcine or avian animal.
 - 8. The isolated or recombinant polypeptide of claim 6 capable of conferring a protective immune response against *Lawsonia spp.* in a porcine or avian animal.
- 15 9. The isolated or recombinant polypeptide of claim 8, capable of inducing humoral immunity against *Lawsonia spp.* in a porcine or avian animal.
 - 10. The isolated or recombinant polypeptide of claim 9, capable of inducing humoral immunity against *Lawsonia spp.* in a porcine animal.
 - 11. The isolated or recombinant polypeptide of claim 7 wherein the *Lawsonia spp*. is *Lawsonia intracellularis*.
- 12. The isolated or recombinant polypeptide of claim 8 wherein the *Lawsonia spp.*25 is *Lawsonia intracellularis*.
 - 13. The isolated or recombinant polypeptide of claim 6 comprising an amino acid sequence selected from the group consisting of:
 - (i) an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, and 18; and
 - (ii) an amino acid sequence encoded by Lawsonia intracellularis DNA

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contained within a deposited plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN).

- 14. The isolated or recombinant polypeptide of claim 13 capable of eliciting the production of antibodies against *Lawsonia intracellularis* when administered to an avian or porcine animal.
- 15. The isolated or recombinant polypeptide of claim 13 capable of inducing a protective immune response against *Lawsonia intracellularis* in a porcine or avian animal.
- 16. The isolated or recombinant polypeptide of claim 15 capable of inducing a protective immune response against *Lawsonia intracellularis* in a porcine animal.
- 17. A vaccine composition for the prophylaxis or treatment of infection of an animal by Lawsonia spp., said vaccine composition comprising an immunogenic component which comprises the isolated or recombinant immunogenic polypeptide according to claim 1 in combination with one or more carriers, diluents or adjuvants suitable for veterinary or pharmaceutical use.
 - 18. The vaccine composition according to claim 17 wherein the *Lawsonia spp.* is *Lawsonia intracellularis*.
- 19. The vaccine composition according to claim 17 wherein the immunogenic component comprises an isolated or recombinant polypeptide having an amino acid sequence selected from the group consisting of:

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- (i) an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, and 18; and
- (ii) an amino acid sequence encoded by Lawsonia intracellularis DNA contained within a deposited plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN);
- 20. The vaccine composition of claim 17, wherein the immunogenic component is a recombinant polypeptide expressed in a cell that has been transfected with a vector comprising a nucleotide sequence selected from the group consisting of:
 - (i) a protein-encoding nucleotide sequence having at least about 60% sequence identity overall to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, and 17;
 - (ii) a protein-encoding nucleotide sequence having at least about 60% sequence identity overall to the protein-encoding sequence of *Lawsonia intracellularis* DNA contained within a plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN);
- 25 (iii) a protein-encoding nucleotide sequence which comprises at least about 15 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, and 17;
 - (iv)a protein-encoding nucleotide sequence which comprises at least about 15 contiguous nucleotides of the protein-encoding sequence of *Lawsonia intracellularis* DNA contained within a plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH);

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NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN);

- (v) a protein-encoding nucleotide sequence which hybridizes under at least low stringency conditions to the complement of a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, and 17; (vi)a protein-encoding nucleotide sequence which hybridizes under at least low stringency conditions to the non-coding strand of *Lawsonia intracellularis* DNA contained within a p plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN); and
- (vii) a homologue, analogue or derivative of any one of (i) to (vi) which encodes a polypeptide which mimics a B-cell or T-cell epitope of *Lawsonia spp*.
- 21. A combination vaccine composition for the prophylaxis or treatment of infection of an animal by *Lawsonia spp.*, said vaccine composition comprising:
 - (i) a first immunogenic component which comprises the isolated or recombinant polypeptide having according to claim 1;
 - (ii) a second immunogenic component different from said first immunogenic component and comprising a polypeptide selected from the group consisting of the *Lawsonia intracellularis* FlgE, hemolysin, OmpH, SodC, flhB, fliR, ntrC, glnH, motA, motB, tlyC, ytfM, and ytfN polypeptides; and
 - (iii) one or more carriers, diluents or adjuvants suitable for veterinary or pharmaceutical use.
- 30 22. A vaccine vector that comprises, in an expressible form, an isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

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- (i) a protein-encoding nucleotide sequence having at least about 60% sequence identity overall to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, and 17;
- (ii) a protein-encoding nucleotide sequence having at least about 60% sequence identity overall to the protein-encoding sequence of *Lawsonia intracellularis* DNA contained within a plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN);
- (iii) a protein-encoding nucleotide sequence which comprises at least about 15 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, and 17;
- (iv) a protein-encoding nucleotide sequence which comprises at least about 15 contiguous nucleotides of the protein-encoding sequence of *Lawsonia intracellularis* DNA contained within a plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN);
- (v) a protein-encoding nucleotide sequence which hybridizes under at least low stringency conditions to the complement of a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, and 17; (vi)a protein-encoding nucleotide sequence which hybridizes under at least low stringency conditions to the non-coding strand of *Lawsonia intracellularis* DNA contained within a plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid

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pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN); and

- (vii) a homologue, analogue or derivative of any one of (i) to (vi) which encodes a polypeptide which mimics a B-cell or T-cell epitope of *Lawsonia spp*. wherein said vaccine vector expresses the polypeptide encoded by said nucleotide sequence at a level sufficient to confer immunity against *Lawsonia spp*. when administered to a porcine or avian animal.
- 23. The vaccine vector of claim 22 wherein the immunogenic polypeptide is expressed by a process comprising:
 - (i) placing an isolated nucleic acid molecule in an expressible format, said nucleic acid molecule comprising the coding region of a gene selected from the group consisting of *flhB*, *fliR*, *ntrC*, *glnH*, *motA*, *motB*, *tlyC*, *ytfM*, and *ytfN* genes, or a protein-encoding homologue, analogue or derivative thereof;
 - (ii) introducing the isolated nucleic acid molecule of (i) in an expressible format into a suitable vaccine vector; and
 - (iii) incubating or growing the vaccine vector for a time and under conditions sufficient for expression of the immunogenic component encoded by said nucleic acid molecule to occur.
 - 24. The vaccine vector of claim 22 wherein the Lawsonia spp. is L. intracellularis.
 - 25. An isolated polyclonal antibody or a monoclonal antibody molecule that binds specifically to a *Lawsonia spp.* polypeptide selected from the group consisting of flhB, fliR, ntrC, glnH, motA, motB, tlyC, ytfM, and ytfN polypeptides, or a homologue, analogue or derivative of any one or more of said polypeptides.
 - 26. The isolated polyclonal antibody or a monoclonal antibody molecule of claim 25 wherein the polypeptide or derivative thereof comprises an amino acid sequence selected from the group consisting of:
 - (i) an amino acid sequence of Lawsonia sp. which has at least about 60%

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sequence identity overall to a sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, and 18;

- (ii) an amino acid sequence of *Lawsonia sp.* which has at least about 60% sequence identity overall to a sequence encoded by *L. intracellularis* DNA contained within a plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN);
- (iii) an amino acid sequence which comprises at least about 5 contiguous amino acids of a sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, and 18;
- (iv)an amino acid sequence which comprises at least about 5 contiguous amino acids of a sequence encoded by *L. intracellularis* DNA contained within a plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN);
- (v) an amino acid sequence which is encoded by a nucleotide sequence having at least about 60% sequence identity overall to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, and 17;
- (vi)an amino acid sequence which is encoded by a nucleotide sequence having at least about 60% sequence identity overall to the nucleotide sequence of *L. intracellularis* DNA contained within a plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC);

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NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN);

- (vii) an amino acid sequence which is encoded by at least about 15 contiguous nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, and 17;
- (viii) an amino acid sequence which is encoded by at least about 15 contiguous nucleotides of a nucleotide sequence of *L. intracellularis* DNA contained within a plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN); and
- (ix) a homologue, analogue or derivative of any one of (i) to (viii) which mimics a B-cell or T-cell epitope of *Lawsonia spp*.
- 27. A method of diagnosing infection of a porcine or avian animal by *Lawsonia* intracellularis or a microorganism that is immunologically cross-reactive thereto, said method comprising the steps of contacting a biological sample derived from said animal with the antibody molecule of claim 25 for a time and under conditions sufficient for an antigen:antibody complex to form, and then detecting said complex formation.
- 28. The method of claim 27 wherein the biological sample comprises whole serum, lymph nodes, ileum, caecum, small intestine, large intestine, faeces or a rectal swab derived from a porcine animal.
 - 29. A method of identifying whether or not a porcine or avian animal has suffered from a past infection, or is currently infected, with *Lawsonia intracellularis* or a microorganism that is immunologically cross-reactive thereto, said method comprising contacting blood or serum derived from said animal with the immunogenic

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polypeptide of claim 1 for a time and under conditions sufficient for an antigen:antibody complex to form and then detecting said complex formation.

- 30. An isolated nucleic acid molecule which consists of a nucleotide sequence encoding a *Lawsonia spp.* polypeptide selected from the group consisting of flhB, fliR, ntrC, glnH, motA, motB, tlyC, ytfM, and ytfN.
 - 31. The isolated nucleic acid molecule according to claim 30 comprising a sequence of nucleotides selected from the group consisting of:
- (i) a nucleotide sequence having at least about 60% sequence identity overall to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, and 17;
 - (ii) a nucleotide sequence having at least about 60% sequence identity overall to *L. intracellularis* DNA contained within a plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and;
- 20 (iii) a nucleotide sequence which comprises at least about 15 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, and 17;
 - (iv)a nucleotide sequence which comprises at least about 15 contiguous nucleotides of *L. intracellularis* DNA contained within a plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN);
- 30 (v) a nucleotide sequence which hybridizes under at least low stringency conditions to a nucleotide sequence selected from the group consisting of SEQ

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ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, and 17 or a complementary nucleotide sequence thereto;

- (vi)a nucleotide sequence which hybridizes under at least low stringency conditions to *L. intracellularis* DNA contained within a plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN); and
- 10 (vii) a homologue, analogue or derivative of any one of (i) to (vi) which encodes a polypeptide which mimics a B-cell or T-cell epitope of *Lawsonia spp*.
 - 32. The isolated nucleic acid molecule of claim 31 comprising a nucleotide sequence selected from the group consisting of:
 - (i) a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1,3, 5, 7, 9, 11, 13, 15, and 17;
 - (ii) a nucleotide sequence of the *L. intracellularis* DNA contained within a deposited plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN);
 - (iii) a nucleotide sequence that encodes the same polypeptide as a nucleotide sequence of (i) or (ii), wherein said polypeptide is selected from the group consisting of flhB, fliR, ntrC, glnH, motA, motB, tlyC, ytfM, and ytfN polypeptides; and
 - (iv) a nucleotide sequence that is complementary to (i) or (ii) or (iii).
- 30 33. The isolated nucleic acid molecule of claim 32 consisting of the proteinencoding region of (i) or (ii).

- 34. A method of detecting *Lawsonia intracellularis* or related microorganism in a biological sample derived from a porcine or avian animal subject, said method comprising the steps of hybridising one or more probes or primers to said sample and then detecting said hybridisation using a detection means, wherein said probes or primers are derived from a *Lawsonia spp.* gene selected from the group consisting of *flhB*, *fliR*, *ntrC*, *glnH*, *motA*, *motB*, *tlyC*, *ytfM*, and *ytfN* genes.
- 35. The method of claim 34 wherein the biological sample comprises whole serum, lymph nodes, ileum, caecum, small intestine, large intestine, faeces or a rectal swab derived from a porcine animal.
 - 36. The method of claim 34 wherein the detection means comprises any nucleic acid based hybridisation or amplification reaction.
 - 37. A probe or primer comprising a nucleotide sequence selected from the group consisting of:
 - (i) any one of SEQ ID NOs: 19 to 68; and
 - (ii) a complementary nucleotide sequence to (i).

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- 38. A plasmid selected from the group consisting of AGAL Accession Nos: NM00/16476 (plasmid pGTE#1 glnH); NM00/16477 (plasmid pGTE#2 flhB); NM00/16478 (plasmid pGTE#3 fliR); NM00/16479 (plasmid pGTE#4 motA/B); NM00/16480 (plasmid pGTE#5 tlyC); NM00/16481 (plasmid pGTE#6 ntrC); NM00/16482 (plasmid pGTE#7 ytfM); and NM01/23286 (plasmid pGTE#8 ytfN).
- 39. A recombinant vector capable of replication in a host cell, wherein said vector comprises the isolated nucleic acid of claim 30.
- 40. A recombinant vector capable of replication in a host cell, wherein said vector

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comprises the isolated nucleic acid of claim 31.

- 41. A recombinant vector capable of replication in a host cell, wherein said vector comprises the isolated nucleic acid of claim 32.
- 42. A recombinant vector capable of replication in a host cell, wherein said vector comprises the isolated nucleic acid of claim 33.
- 43. A host cell comprising the recombinant vector of claim 39.
- 44. The host cell of claim 43 wherein said host cell is a bacterium.
- 45. A host cell comprising the recombinant vector of claim 40.
- 15 46. The host cell of claim 45 wherein said host cell is a bacterium.
 - 47. A host cell comprising the recombinant vector of claim 41.
 - 48. The host cell of claim 47 wherein said host cell is a bacterium.
 - 49. A host cell comprising the recombinant vector of claim 42.
 - 50. The host cell of claim 49 wherein said host cell is a bacterium.